

Fig. 1

(A) FBD(1,2) fused at the C-terminal of SK

SK			1	2
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(B) FBD(4,5) fused at the C-terminal of SK

SK			4	5
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(C) FBD(4,5) fused at the N-terminal of SK

4	5	SK		
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(D) FBD(4,5) fused at both the C as well as N-terminals of SK

4	5	SK			4	5
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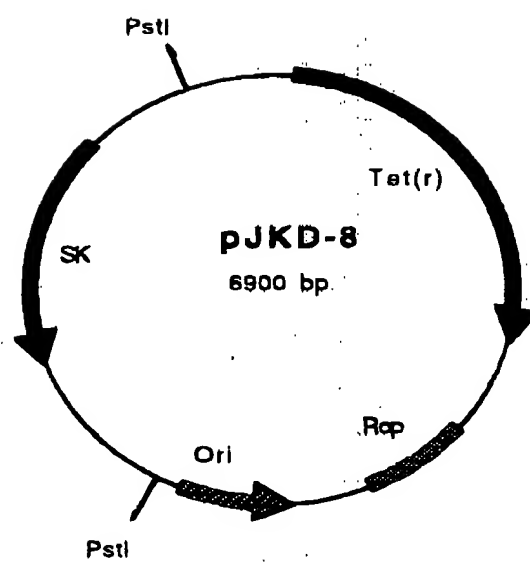
Fig. 2

Fig. 3

1/1  
ATT GCT GGA CCT GAG TGG CTG CTA GAC CGT CCA TCT GTC AAC AAC AGC CAA TTA GTT GTT  
ile ala gly pro glu trp leu leu asp arg pro ser val asn asn ser gln leu val val  
61/21  
AGC GTT GCT GGT ACT GTT GAG GGG ACG AAT CAA GAC ATT AGT CTT AAA TTT TTT GAA ATC  
ser val ala gly thr val glu gly thr asn gln asp ile ser leu lys phe phe glu ile  
121/41  
GAT CTA ACA TCA CGA CCT GCT CAT GGA GGA AAG ACA GAG CAA GGC TTA AGT CCA AAA TCA  
asp leu thr ser arg pro ala his gly gly lys thr glu gln gly leu ser pro lys ser  
181/61  
AAA CCA TTT GCT ACT GAT AGT GGC GCG ATG TCA CAT AAA CTT GAG AAA GCT GAC TTA CTA  
lys pro phe ala thr asp ser gly ala met ser his lys leu glu lys ala asp leu leu  
241/81  
AAG GCT ATT CAA GAA CAA TTG ATC GCT AAC GTC CAC AGT AAC GAC GAC TAC TTT GAG GTC  
lys ala ile gln glu gln leu ile ala asn val his ser asn asp asp tyr phe glu val  
301/101  
ATT GAT TTT GCA AGC GAT GCA ACC ATT ACT GAT CGA AAC GGC AAG GTC TAC TTT GCT GAC  
ile asp phe ala ser asp ala thr ile thr asp arg asn gly lys val tyr phe ala asp  
361/121  
AAA GAT GGT TCG GTA ACC TTG CCG ACC CAA CCT GTC CAA GAA TTT TTG CTA AGC CGA CAT  
lys asp gly ser val thr leu pro thr gln pro val gln glu phe leu leu ser gly his  
421/141  
GTG CCG GTT ACA CCA TAT AAA GAA AAA CCA ATA CAA AAC CAA GCG AAA TCT GTT GAT GTG  
val arg val arg pro tyr lys glu lys pro ile gln asn gln ala lys ser val asp val  
481/161  
GAA TAT ACT GTA CAG TTT ACT CCC TTA AAC CCT GAT GAC GAT TTC AGA CCA GGT CTC AAA  
glu tyr thr val gln phe thr pro leu asn pro asp asp asp phe arg pro gly leu lys  
541/181  
GAT ACT AAG CTA TTG AAA ACA CTA GCT ATC GGT GAC ACC ATC ACA TCT CAA GAA TTA CTA  
asp thr lys leu leu lys thr leu ala ile gly asp thr ile thr ser gln glu leu leu  
601/201  
CCT CAA CCA CAA AGC ATT TTA AAC AAA AAC CAC CCA GCG TAT ACG ATT TAT GAA CGT GAC  
ala gln ala gln ser ile leu asn lys asn his pro gly tyr thr ile tyr glu arg asp  
661/221  
TCC TCA ATC GTC ACT CAT GAC AAT GAC ATT TTC CGT ACG ATT TTA CCA ATG GAT CAA GAG  
ser ser ile val thr his asp asn asp ile phe arg thr ile leu pro met asp gln glu  
721/241  
TTT ACT TAC CGT GTT AAA AAT CCG GAA CAA GCT TAT ACG ATC AAT AAA AAA TCT GGT CTG  
phe thr tyr arg val lys asn arg glu gln ala tyr arg ile asn lys lys ser gly leu  
781/261  
AAT CAA GAA ATA AAC AAC ACT GAC CTG ATC TCT GAG AAA TAT TAC GTC CTT AAA AAA GCG  
asn glu glu ile asn asn thr asp leu ile ser glu lys tyr tyr val leu lys lys gly  
841/281  
GAA AAG CCG TAT GAT CCC TTT GAT CCG AGT CAC TTG AAA CTG TTC ACC ATC AAA TAC GTT  
glu lys pro tyr asp pro phe asp arg ser his leu lys leu phe thr ile lys tyr val  
901/301  
GAT GTC GAT ACC AAC GAA TTG CTA AAA AGT GAG CAG CTC TTA ACA GCT AGC GAA CGT AAC  
asp val asp thr asn glu leu leu lys ser glu gln leu leu thr ala ser glu arg asn  
961/321  
TTA GAC TTC AGA GAT TTA TAC GAT CCT CGT GAT AAG GCT AAA CTA CTC TAC AAC AAT CTC  
leu asp phe arg asp leu tyr asp pro arg asp lys ala lys leu leu tyr asn asn leu  
1021/341  
GAT GCT TTT GGT ATT ATG GAC TAT ACC TTA ACT GGA AAA GTA GAG GAT AAT CAC GAT GAC  
asp ala phe gly ile met asp tyr thr leu thr gly lys val glu asp asn his asp asp  
1081/361  
ACC AAC CGT ATC ATA ACC GTT TAT ATG GGC AAG CCA CCC GAA GGA GAG AAT GCT AGC TAT  
thr asn arg ile ile thr val tyr met gly lys arg pro glu gly glu asn ala ser tyr  
1141/381  
CAT TTA GCC TAT GAT AAA GAT CGT TAT ACC GAA GAA GAA CGA GAA GTT TAC AGC TAC CTG  
his leu ala tyr asp lys asp arg tyr thr glu glu glu arg glu val tyr ser tyr leu  
1201/401  
CGT TAT ACA GCG ACA CCT ATA CCT GAT AAC CCT AAC GAC AAA TAA  
arg tyr thr gly thr pro ile pro asp asn pro asn asp lys OCH  
1231/411

Fig. 4

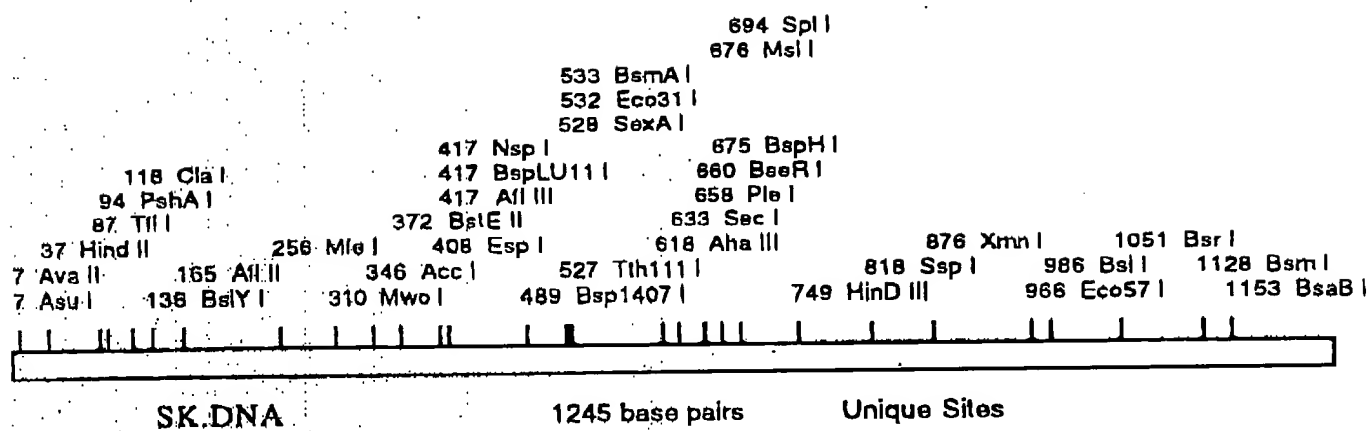


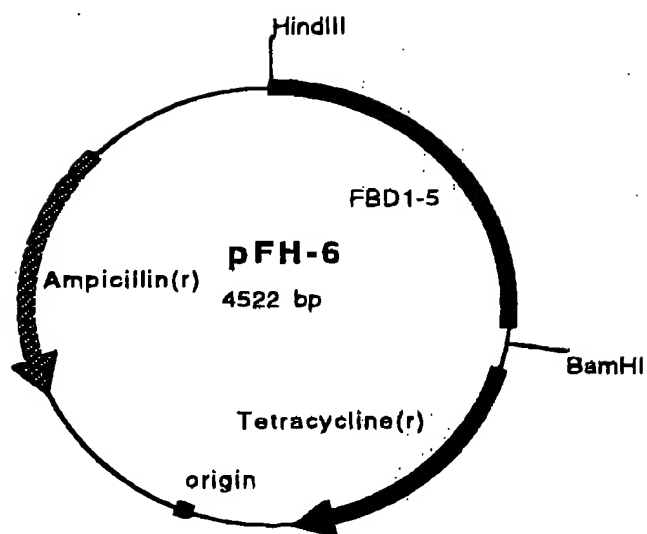
Fig. 5

Fig. 6

1/1  
 CAG GCT CAG CAA ATG GTT CAG CCC CAG TCC CCG GTG GCT GTC ACT CAA AGC AAG CCC GGT  
 gln ala gln gln met val gln pro gln ser pro val ala val ser gln ser lys pro gly  
 61/21  
 TGT TAT GAC AAT GGA AAA CAC TAT CAG ATA AAT CAA CAG TGG GAG CCG ACC TAC CTA GGT  
 cys tyr asp asn gly lys his tyr gln ile asn gln gln trp glu arg thr tyr leu gly  
 121/41  
 AAT CTC TTG GTT TGT ACT TGT TAT GGA GGA AGC CGA GGT TTT AAC TGC GAA AGT AAA CCT  
 asn val leu val cys thr cys tyr gly gly ser arg gly phe asn cys glu ser lys pro  
 181/61  
 GAA GCT GAA GAG ACT TGC TTT GAC AAG TAC ACT GGG AAC ACT TAC CGA GTG GGT GAC ACT  
 glu ala glu glu thr cys phe asp lys tyr thr gly asn thr tyr arg val gly asp thr  
 241/81  
 TAT GAG CGT CCT AAA GAC TCC ATG ATC TGG GAC TGT ACC TGC ATC GGG GCT GGG CGA GGG  
 tyr glu arg pro lys asp ser met ile trp asp cys thr cys ile gly ala gly arg gly  
 301/101  
 AGA ATA AGC TGT ACC ATC GCA AAC CGC TGC CAT GAA GGG GGT CAG TCC TAC AAG ATT GGT  
 arg ile ser cys thr ile ala asn arg cys his glu gly gly gln ser tyr lys ile gly  
 361/121  
 GAC ACC TGG AGG AGA CCA CAT GAG ACT GGT GGT TAC ATG TTA GAG TGT GTG TGT CTT GGT  
 asp thr trp arg arg pro his glu thr gly gly tyr met leu glu cys val cys leu gly  
 421/141  
 AAT GGA AAA GGA GAA TGG ACC TGC AAG CCC ATA GCT GAG AAG TGT TTT GAT CAT GCT GCT  
 asn gly lys gly glu trp thr cys lys pro ile ala glu lys cys phe asp his ala ala  
 481/161  
 GGC ACT TCC TAT GTG GTC GGA GAA ACG TGG GAG AAG CCC TAC CAA GGC TGG ATG ATG GTA  
 gly thr ser tyr val val gly glu thr trp glu lys pro tyr gln gly trp met met val  
 541/181  
 GAT TGT ACT TGC CTG GGA GAA GGC AGC GGA CGC ATC ACT TGC ACT TCT AGA AAT AGA TGC  
 asp cys thr cys leu gly glu gly ser gly arg ile thr cys thr ser arg asn arg cys  
 601/201  
 AAC GAT CAG GAC ACA AGG ACA TCC TAT AGA ATT GGA GAC ACC TGG ACC AAG AAG GAT AAT  
 asn asp gln asp thr arg thr ser tyr arg ile gly asp thr trp ser lys lys asp asn  
 661/221  
 CGA GGA AAC CTG CTC CAG TGC ATC TGC ACA CGC AAC GGC CGA CGA GAG TGG AAG TGT GAG  
 arg gly asn leu leu gln cys ile cys thr gly asn gly arg gly glu trp lys cys glu  
 721/241  
 AGG CAC ACC TCT GTG CAG ACC ACA TCG AGC GGA TCT GGC CCC TTC ACC GAT GTT CGT  
 arg his thr ser val gln thr thr ser ser gly ser gly pro phe thr asp val arg

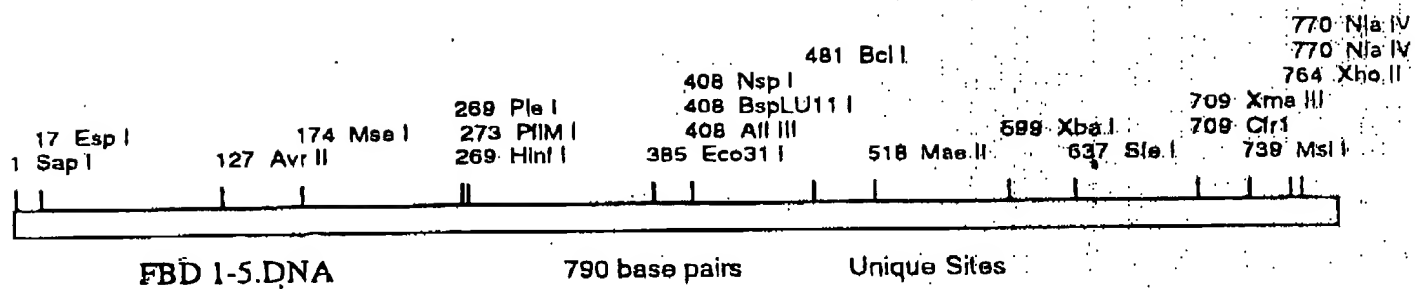
Fig. 7

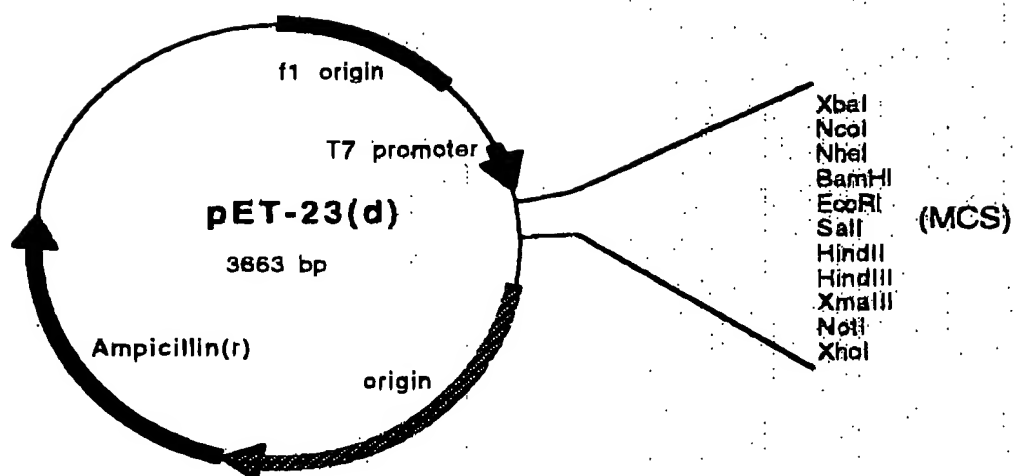
Fig. 8



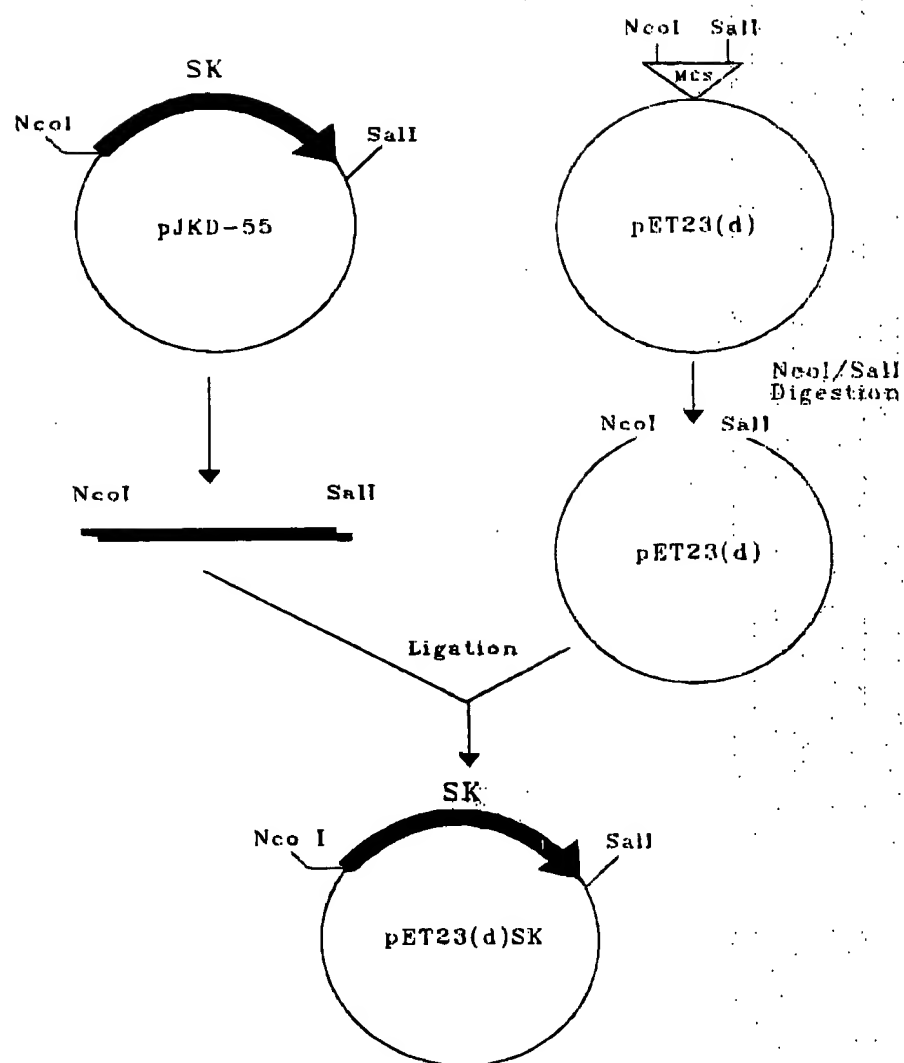
Fig. 9

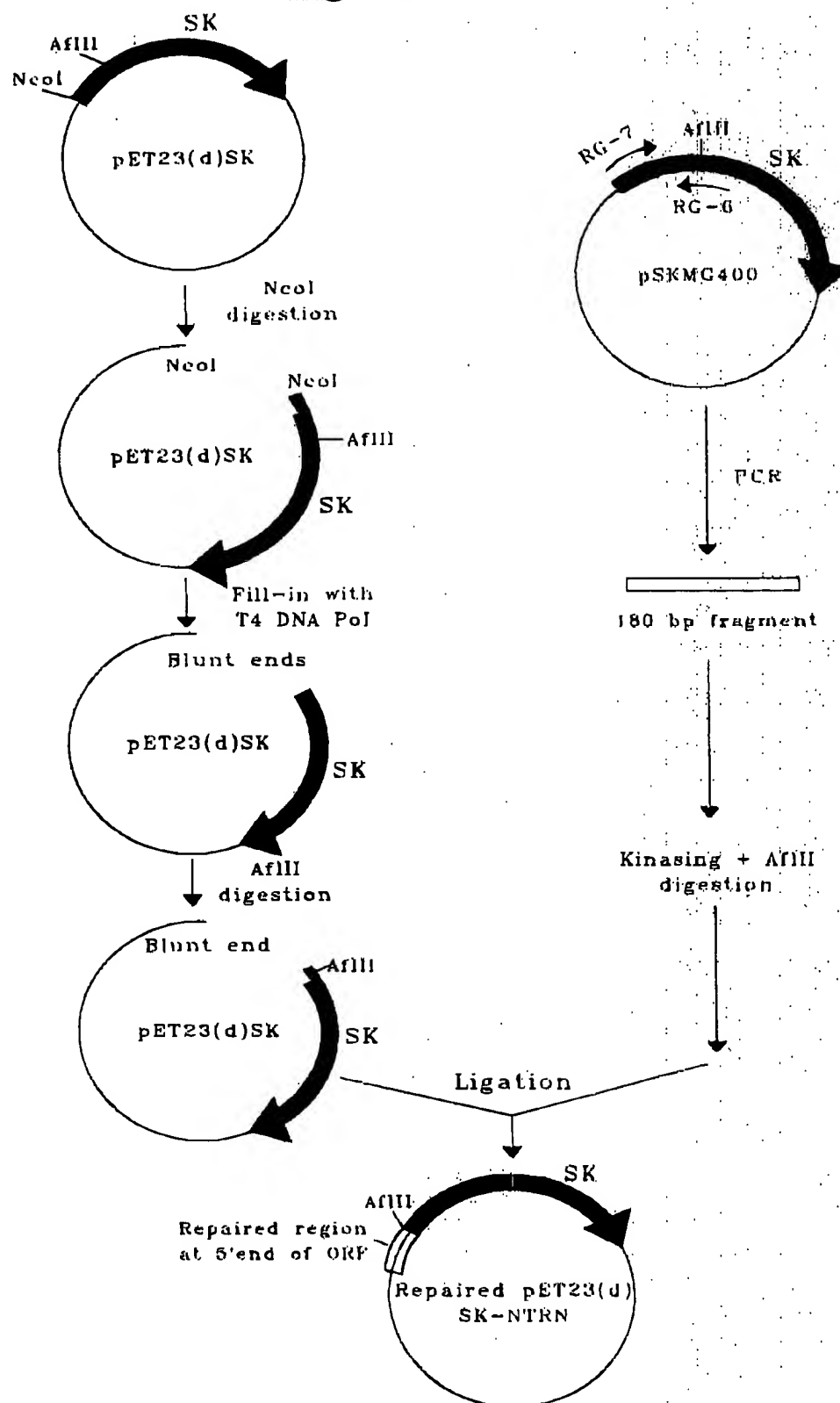
Fig. 10

Fig. 11

	10	20	30	40	50
	GCACCCGTGG	CCAGGACCCA	ACGCTGCCCG	AGATCTCGAT	CCCCCGAAAT
51	TAATACGACT	CACTATAGGG	AGACCACAAC	GGTTCCCTC	TAGAAATAAT
101	TTTGTTTAAC	TTTAAGAAGG	AGATATACCA	TGATTGCTGG	ACCTGAGTGG
151	CTGCTAGACC	GTCCATCTGT	CAACAACAGC	CAATTGGTTG	TTAGCGTTGC
201	TGGTACTGTT	GAGGGGACGA	ATCAAGACAT	TAGTCTTAAA	TTTTTTGAAA
251	TCGATCTAAC	ATCACGACCT	GCTCATGGAG	GAAAGACAGA	GCAAGGCTTA
301	AGTCCAAAAT	CAAAACCAAT	TGCTACTGAT	AGTGGCGCGA	TGTCACATAA
351	ACTTGAGAAA	GCTGACTTAC	TAAAGGCTAT	TCAAGAACAA	TTGATCGCTA
401	ACGTCCACAG	TAACGACGAC	TACTTTGAGG	TCATTGATTT	TGCAAGCGAT
451	GCAACCATT	CTGATCGAAA	CGGCAAGGTC	TACTTTGCTG	ACAAAGATGG
501	TTCCGGTAACC	TTGCCGACCC	AACCTGTCCA	AGAATTTTGT	CTAAGCGGAC
551	ATGTGCGCGT	TAGACCATAT	AAAGAAAAAC	CAATACAAAA	CCAAGCGAAA
601	TCTGTTGATG	TGGAATATAC	TGTACAGTTT	ACTCCCTTAA	ACCCTGATGA
651	CGATTTTACA	CCAGGTCTCA	AAGATACTAA	GCTATTGAAA	ACACTAGCTA
701	TCGGTGACAC	CATCACATCT	CAAGAATTAC	TAGCTCAAGC	ACAAAGCAAT
751	TTAAACAAAA	ACCACCCAGG	CTATACGATT	TATGAACGTG	ACTCCTCAAT
801	CGTCACTCAT	GACAAAGACA	TTTTCCGTAC	GATTTTACCA	ATGGATCAAG
851	AGTTTACTTA	CCGTGTTAAA	AATCGGGAAC	AAGCTTATAG	GATCAATAAA
901	AAATCTGGTC	TGAATGAAGA	AATAAACAAC	ACTGACCTGA	TCTCTGAGAA
951	ATATTACGTC	CTTAAAAAAG	GGGAAAAGCC	GTATGATCCC	TTTGATCGCA
1001	GTCACCTGAA	ACTGTTCCAC	ATCAAATACG	TTGATGTCGA	TACCAACGAA
1051	TTGCTAAAAA	GTGAGCAGCT	CTTAACAGCT	AGCGAACGTA	ACTTAGACTT
1101	CAGAGATTTA	TACGATCCTC	GTGATAAGGC	TAAACTACTC	TACAACAATC
1151	TCGATGCTTT	TGGTATTATG	GACTATACCT	TAACTGGAAA	AGTAGAGGAT
1201	AATCACGATG	ACACCAACCG	TATCATAACC	GTTTATATGG	GCAAGCGACC
1251	CGAAGGAGAG	AATGCTAGCT	ATCATTTAGC	CTATGATAAA	GATCGTTATA
1301	CCGAAGAAGA	ACGAGAAGTT	TACAGCTACC	TGCGTTATAC	AGGGACACCT
1351	ATACCTGATA	ACCCTAACGA	CAAATAA		



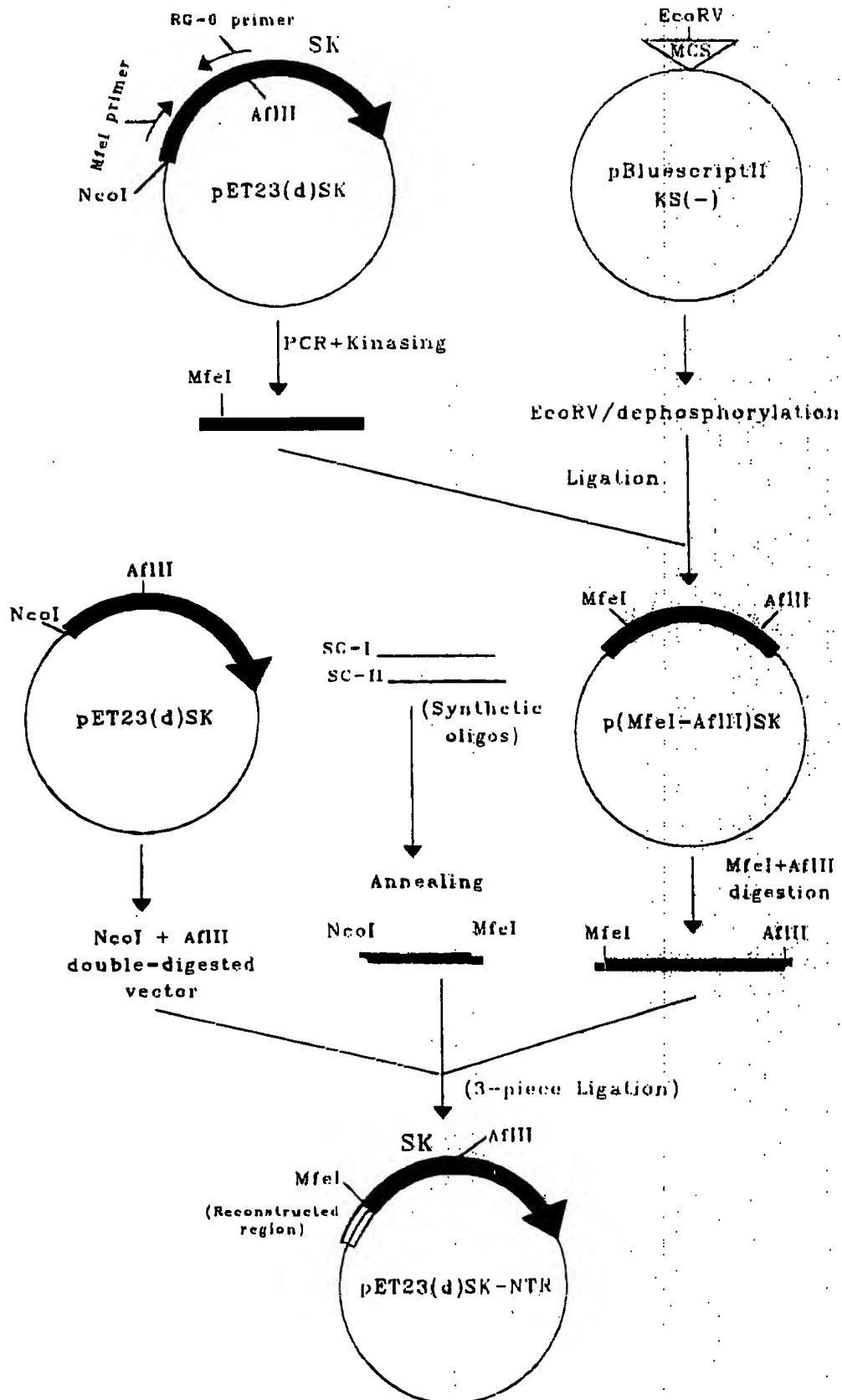
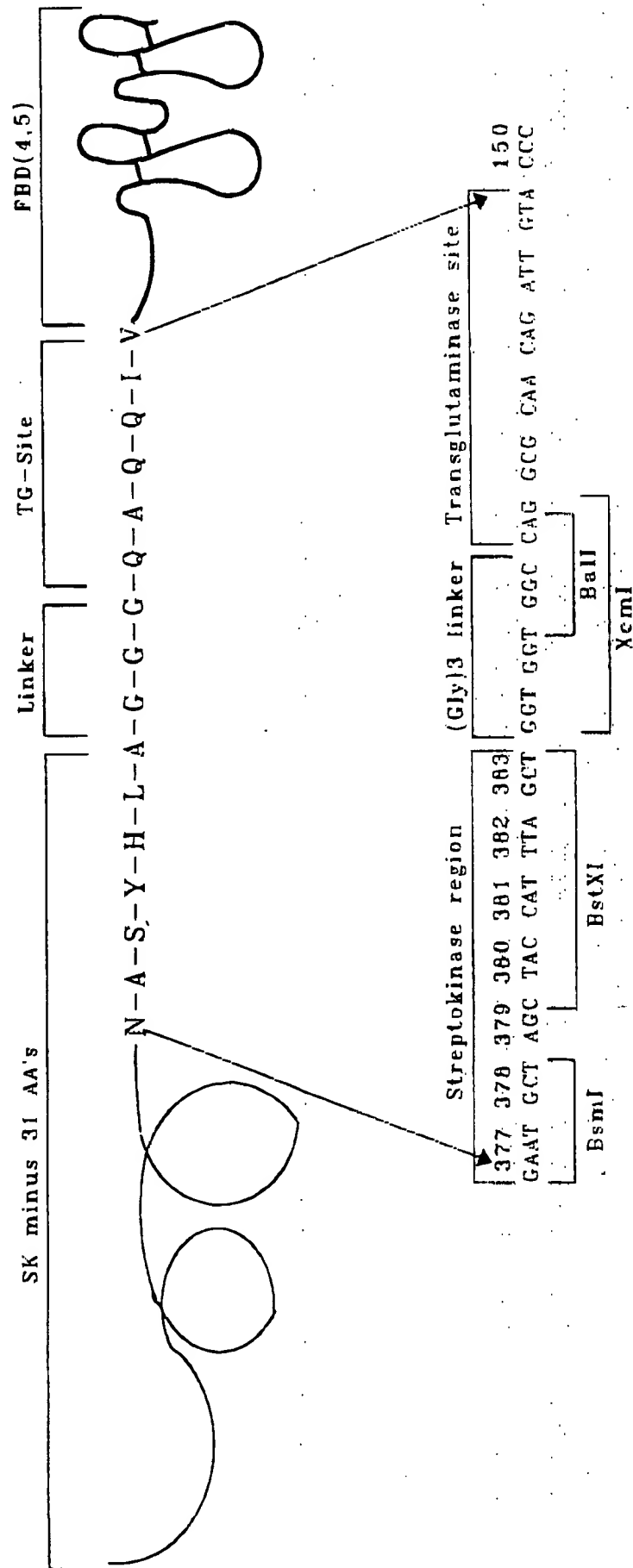
**Fig. 13**

Fig. 14

	10	20	30	40	50
51	TAATACGACT	CACTATAGGG	AGACCACAAC	GGTTTCCCTC	TAGAAATAAT
101	TTTGTTTAAC	TTTAAGAAGG	AGATATACCA	TGATAGCTGG	TCCTGAATGG
151	CTACTAGATC	GTCCTTCTGT	AAATAACAGC	CAATTGGTTG	TTAGCGTTGC
201	TGGTACTGTT	GAGGGGACGA	ATCAAGACAT	TAGTCTTAAA	TTTTTTGAAA
251	TCGATCTAAC	ATCACGACCT	GCTCATGGAG	GAAAGACAGA	GCAAGGCTTA
301	AGTCCAAAAT	CAAAACCATT	TGCTACTGAT	AGTGGCGCGA	TGTCACATAA
351	ACTTGAGAAA	GCTGACTTAC	TAAAGGCTAT	TCAAGAACAA	TTGATCGCTA
401	ACGTCCACAG	TAACGACGAC	TACTTTGAGG	TCATTGATTT	TGCAAGCGAT
451	GCAACCATTA	CTGATCGAAA	CGGCAAGGTC	TACTTTGCTG	ACAAAGATGG
501	TTCGGTAACC	TTGCCGACCC	AACCTGTCCA	AGAATTTTTG	CTAAGCGGAC
551	ATGTGCGCGT	TAGACCATAT	AAAGAAAAAC	CAATACAAAA	CCAAGCGAAA
601	TCTGTTGATG	TGGAATATAC	TGTACAGTTT	ACTCCCTTAA	ACCCTGATGA
651	CGATTTTCAGA	CCAGGTCTCA	AAGATACTAA	GCTATTGAAA	ACACTAGCTA
701	TCGGTGACAC	CATCACATCT	CAAGAATTAC	TAGCTCAAGC	ACAAAGCATT
751	TTAAACAAAA	ACCACCCAGG	CTATACGATT	TATGAACGTG	ACTCCTCAAT
801	CGTCACTCAT	GACAATGACA	TTT TCCGTAC	GATTTTACCA	ATGGATCAAG
851	AGTTTACTTA	CCGTGTTAAA	AATCGGGAAC	AAGCTTATAG	GATCAATAAA
901	AAATCTGGTC	TGAATGAAGA	AATAAACAAC	ACTGACCTGA	TCTCTGAGAA
951	ATATTACGTC	CTTAAAAAAG	GGGAAAAGCC	GTATGATCCC	TTTGATCGCA
1001	GTCAC TTGAA	ACTGTT CACC	ATCAAATACG	TTGATGTCGA	TACCAACGAA
1051	TTGCTAAAAA	GTGAGCAGCT	CTTAACAGCT	AGCGAACGTA	ACTTAGACTT
1101	CAGAGATTTA	TACGATCCTC	GTGATAAGGC	TAAACTACTC	TACAACAATC
1151	TCGATGCTTT	TGGTATTATG	GACTATACCT	TAACTGGAAA	AGTAGAGGAT
1201	AATCACGATG	ACACCAACCG	TATCATAACC	GTTTATATGG	GCAAGCGACC
1251	CGAAGGAGAG	AATGCTAGCT	ATCATTTAGC	CTATGATAAA	GATCGTTATA
1301	CCGAAGAAGA	ACGAGAAGTT	TACAGCTACC	TGCGTTATAC	AGGGACACCT
	ATACCTGATA	ACCCTAACGA	CAAATAA		

**Fig. 15**

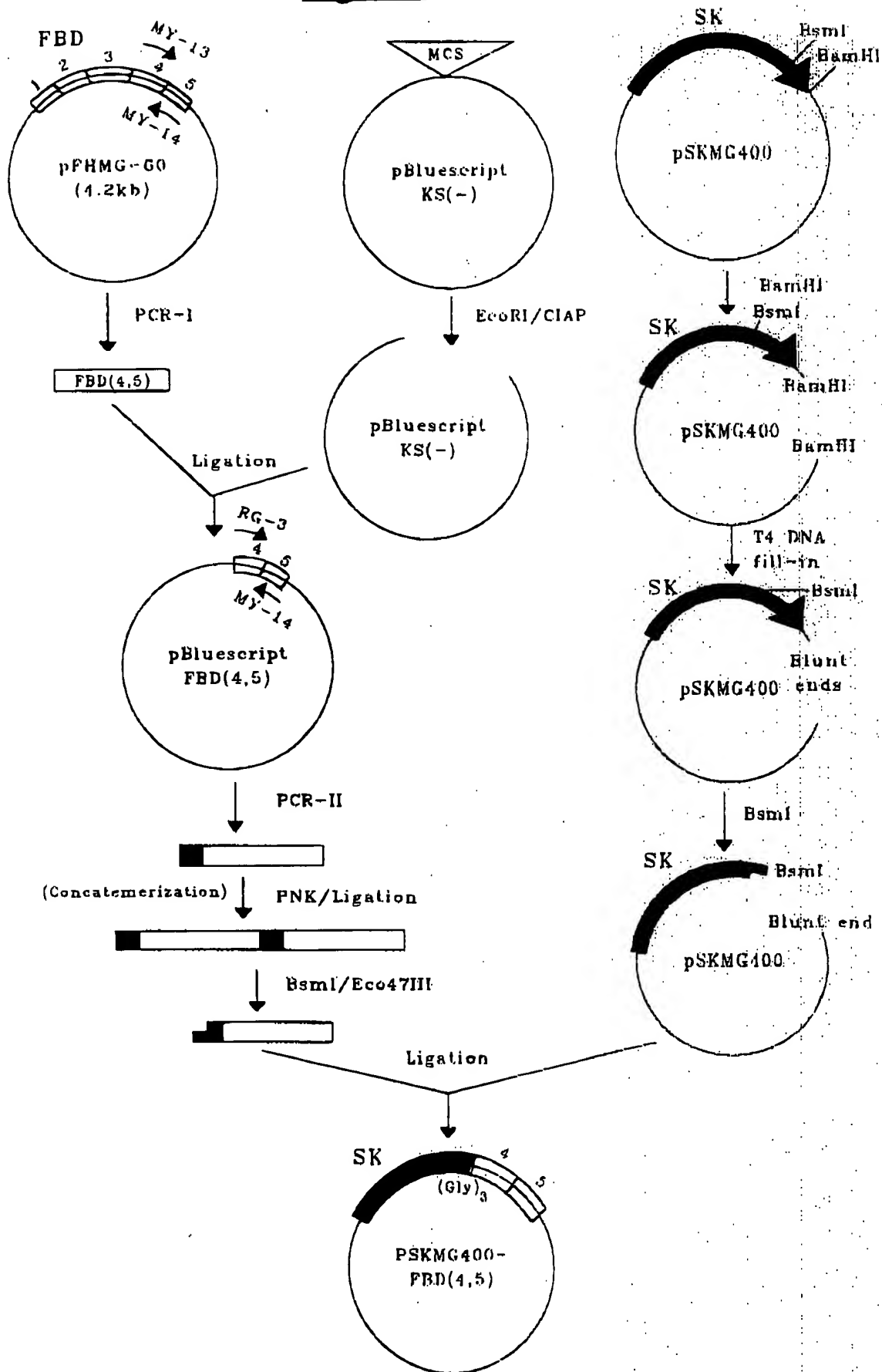
**Fig. 16**



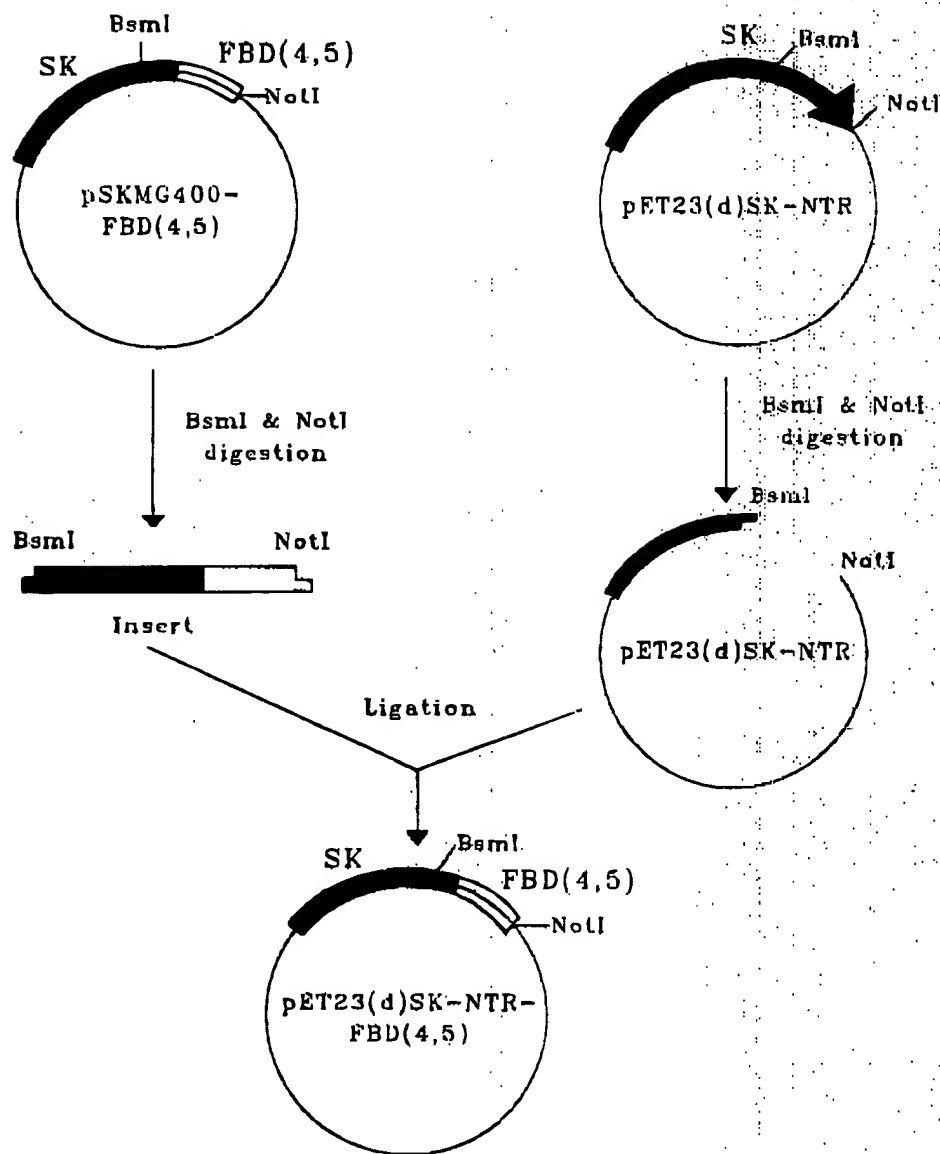
Fig. 17a

Fig. 17b

	10	20	30	40	50
51	TTTGTTTAAC	TTTAAGAAGG	AGATATACCA	TGATAGCTGG	TCCTGAATGG
101	CTACTAGATC	GTCCTTCTGT	AAATAACAGC	CAATTGGTTG	TTAGCGTTGC
151	TGGTACTGTT	GAGGGGACGA	ATCAAGACAT	TAGTCTTAAA	TTTTTTGAAA
201	TCGATCTAAC	ATCACGACCT	GCTCATGGAG	GAAAGACAGA	GCAAGGCTTA
251	AGTCCAAAAT	CAAAACCATT	TGCTACTGAT	AGTGGCGCGA	TGTCACATAA
301	ACTTGAGAAA	GCTGACTTAC	TAAAGGCTAT	TCAAGAACAA	TTGATCGCTA
351	ACGTCCACAG	TAACGACGAC	TACTTTGAGG	TCATTGATTT	TGCAAGCGAT
401	GCAACCATTA	CTGATCGAAA	CGGCAAGGTC	TACTTTGCTG	ACAAAGATGG
451	TTCGGTAACC	TTGCCGACCC	AACCTGTCCA	AGAATTTTGG	CTAAGCGGAC
501	ATGTGCGCGT	TAGACCATAT	AAAGAAAAAC	CAATACAAAA	CCAAGCGAAA
551	TCTGTTGATG	TGGAATATAC	TGTACAGTTT	ACTCCCTTAA	ACCCTGATGA
601	CGATTTTACA	CCAGGTCTCA	AAGATACTAA	GCTATTGAAA	ACACTAGETA
651	TCGGTGACAC	CATCACATCT	CAAGAATTAC	TAGCTCAAGC	ACAAAGCAAT
701	TTAAACAAAA	ACCACCCAGG	CTATACGATT	TATGAACGTG	ACTCCTCAAT
751	CGTCACTCAT	GACAATGACA	TTTTCCGTAC	GATTTTACCA	ATGGATCAAG
801	AGTTTACTTA	CCGTGTTAAA	AATCGGGAAC	AAGCTTATAG	GATCAATAAA
851	AAATCTGGTC	TGAATGAAGA	AATAAACAAC	ACTGACCTGA	TCTCTGAGAA
901	ATATTACGTC	CTTAAAAAAG	GGGAAAAGCC	GTATGATCCC	TTTGATCGCA
951	GTCACCTGAA	ACTGTTCCAC	ATCAAATACG	TTGATGTCGA	TACCAACGAA
1001	TTGCTAAAAA	GTGAGCAGCT	CTTAACAGCT	AGCGAACGTA	ACTTAGACTT
1051	CAGAGATTTA	TACGATCCTC	GTGATAAGGC	TAAACTACTC	TACAACAATC
1101	TCGATGCTTT	TGGTATTATG	GACTATACCT	TAACTGGAAA	AGTAGAGGAT
1151	AATCACGATG	ACACCAACCG	TATCATAACC	GTTTATATGG	GCAAGCGACC
1201	CGAAGGAGAG	AATGCTAGCT	ACCATTTAGC	TGGTGGTGGC	CAGGCGCAAC
1251	AGATTGTACC	CATAGCTGAG	AAGTGTTTTG	ATCATGCTGC	TGGGACTTCC
1301	TATGTGGTCG	GAGAAACGTG	GGAGAAGCCC	TACCAAGGCT	GGATGATGGT
1351	AGATTGTACT	TGCCTGGGAG	AAGGCAGCGG	ACGCATCACT	TGCACTTCTA
1401	GAAATAGATG	CAACGATCAG	GACACAAGGA	CATCCTATAG	AATTGGAGAC
1451	ACCTGGAGCA	AGAAGGATAA	TCGAGGAAAC	CTGCTCCAGT	GCATCTGCAC
1501	AGGCAACGGC	CGAGGAGAGT	GGAAGTGTGA	GAGGCACACC	TCTGTGCAGA
	CCACATCGAG	CGGATCTGGC	CCCTTCACCG	ATGTTTCGTA	G

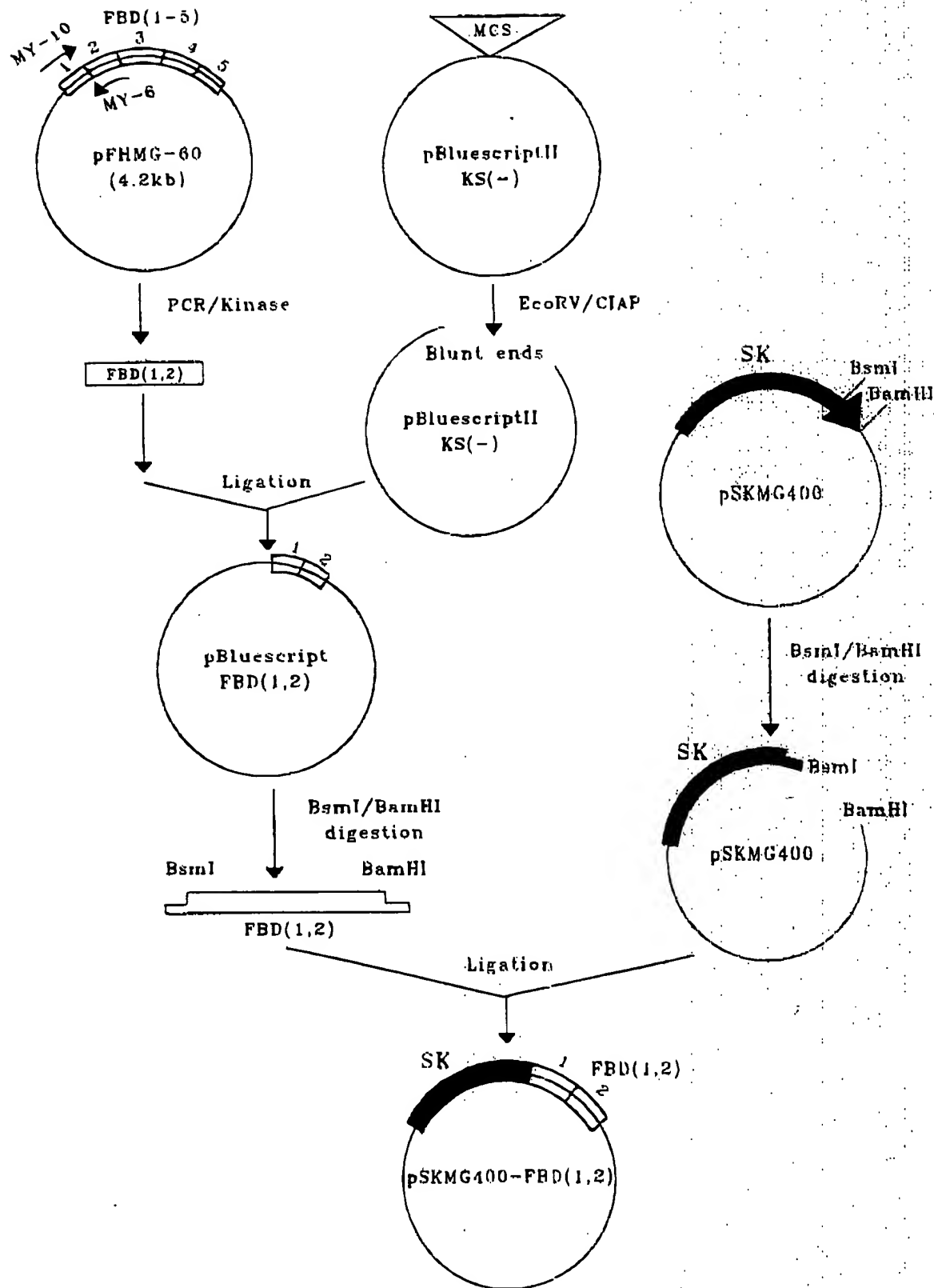
Fig. 18

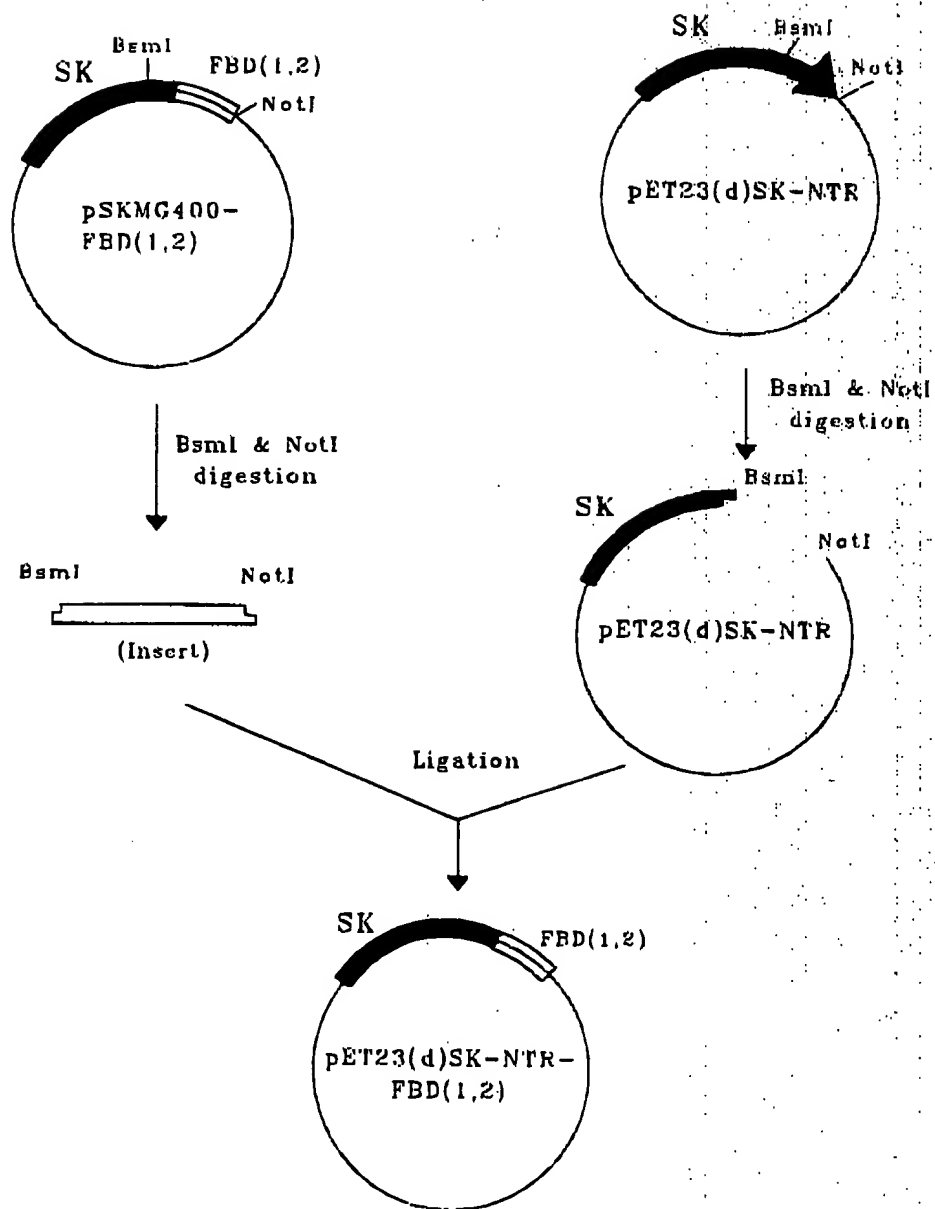
Fig. 19a

Fig. 19b

	10	20	30	40	50
	GCAACCCCGC	CAGCCTAGCC	GGGTCCTCAA	CGACAGGAGC	ACGATCATGC
51	GCACCCGTGG	CCAGGACCCA	ACGCTGCCCG	AGATCTCGAT	CCCGCGAAAT
101	TAATACGACT	CACTATAGGG	AGACCACAAC	GGTTTCCCTC	TAGAAATAAT
151	TTTGTTTAAC	TTTAAGAAGG	AGATATACCA	TGATTGCTGG	ACCTGAGTGG
201	CTGCTAGACC	GTCCATCTGT	CAACAACAGC	CAATTGGTTG	TTAGCGTTGC
251	TGGTACTGTT	GAGGGGACGA	ATCAAGACAT	TAGTCTTAAA	TTTTTTGAAA
301	TCGATCTAAC	ATCACGACCT	GCTCATGGAG	GAAAGACAGA	GCAAGGCTTA
351	AGTCCAAAAT	CAAAACCATT	TGCTACTGAT	AGTGGCGCGA	TGTCACATAA
401	ACTTGAGAAA	GCTGACTTAC	TAAAGGCTAT	TCAAGAACAA	TTGATCGCTA
451	ACGTCCACAG	TAACGACGAC	TACTTTGAGG	TCATTGATTT	TGCAAGCGAT
501	GCAACCATT	CTGATCGAAA	CGGCAAGGTC	TACTTTGCTG	ACAAAGATGG
551	TTCGGTAACC	TTGCCGACCC	AACCTGTCCA	AGAATFTTTG	CTAAGCGGAC
601	ATGTGCGCGT	TAGACCATAT	AAAGAAAAAC	CAATACAAAA	CCAAGCGAAA
651	TCTGTTGATG	TGGAATATAC	TGTACAGTTT	ACTCCCTTAA	ACCCTGATGA
701	CGATTTTACA	CCAGGTCTCA	AAGATACTAA	GCTATTGAAA	ACACTAGCTA
751	TCGGTGACAC	CATCACATCT	CAAGAATTAC	TAGCTCAAGC	ACAAAGCATT
801	TTAAACAAAA	ACCACCCAGG	CTATACGATT	TATGAACGTG	ACTCCTCAAT
851	CGTCACTCAT	GACAATGACA	TTTTCCGTAC	GATTTTACCA	ATGGATCAAG
901	AGTTTACTTA	CCGTGTTAAA	AATCGGGAAC	AAGCTTATAG	GATCAATAAA
951	AAATCTGGTC	TGAATGAAGA	AATAAACAAC	ACTGACCTGA	TCTCTGAGAA
1001	ATATTACGTC	CTTAAAAAAG	GGGAAAAGCC	GTATGATCCC	TTTGATCGCA
1051	GTCACCTGAA	ACTGTTCAAC	ATCAAATACG	TTGATGTCGA	TACCAACGAA
1101	TTGCTAAAAA	GTGAGCAGCT	CTTAACAGCT	AGCGAACGTA	ACTTAGACTT
1151	CAGAGATTTA	TACGATCCTC	GTGATAAGGC	TAACTACTC	TACAACAATC
1201	TCGATGCTTT	TGGTATTATG	GACTATACCT	TAACTGAAA	AGTAGAGGAT
1251	AATCACGATG	ACACCAACCG	TATCATAACC	GTTTATATGG	GCAAGCGACC
1301	CGAAGGAGAG	AATGCTAGCT	ATCATTTAGC	CGGTGGTGGT	CAGGCGCAGC
1351	AAATGGTTCA	GCCCCAGTCC	CCGGTGGCTG	TCAGTCAAAG	CAAGCCCCGT
1401	TGTTATGACA	ATGGAAAACA	CTATCAGATA	AATCAACAGT	GGGAGCGGAC
1451	CTACCTAGGT	AATGTGTTGG	TTTGTACTTG	TTATGGAGGA	AGCCGAGGTT
1501	TTAACTGCGA	AAGTAAACCT	GAAGCTGAAG	AGACTTGCTT	TGACAAGTAC
1551	ACTGGGAACA	CTTACCGAGT	GGGTGACACT	TATGAGCGTC	CTAAAGACTC
1601	CATGATCTGG	GACTGTACCT	GCATCGGGGC	TGGGCGAGGG	AGAATAAGCT
1651	GTACCATCTA	A			

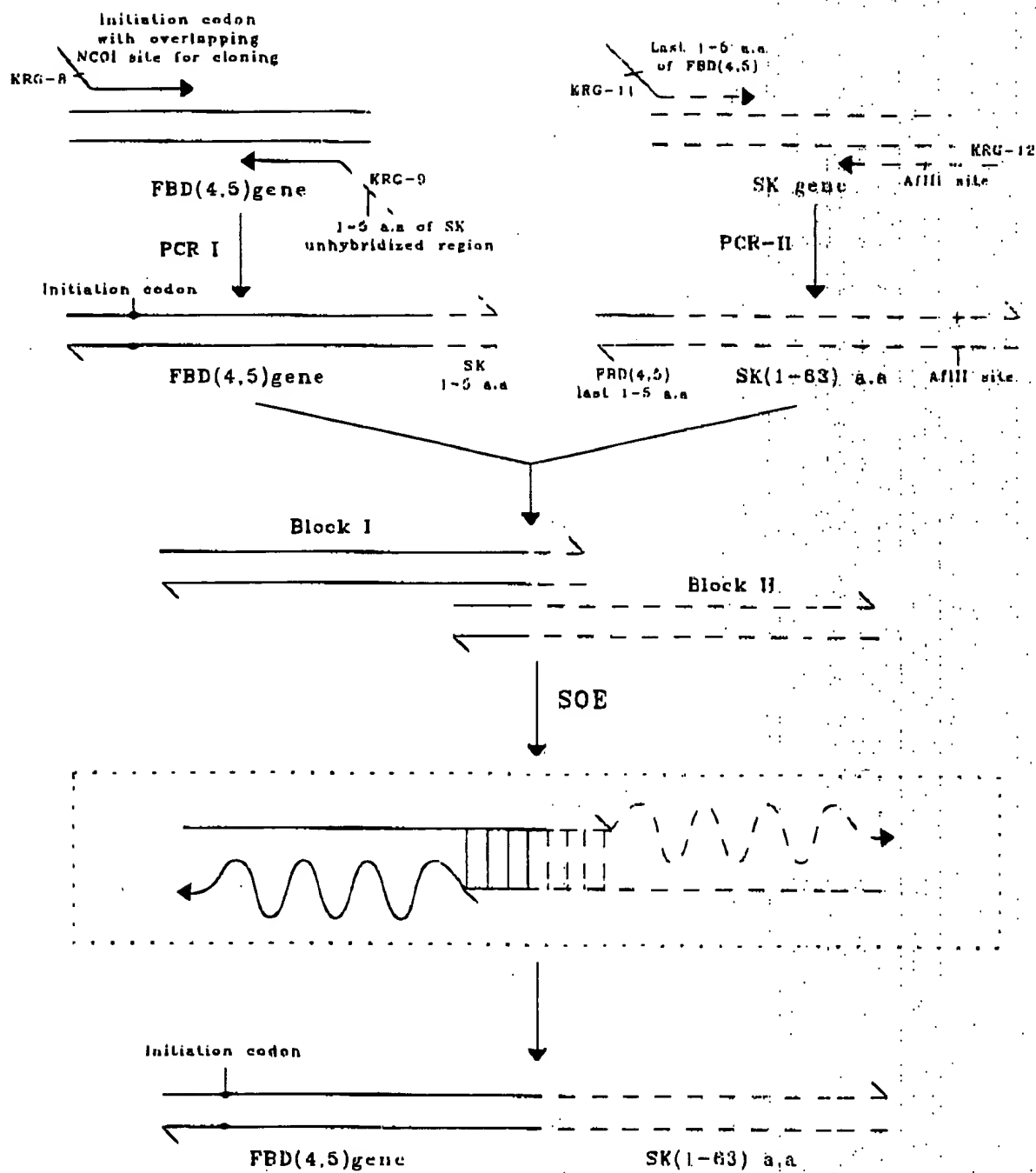
Fig. 20

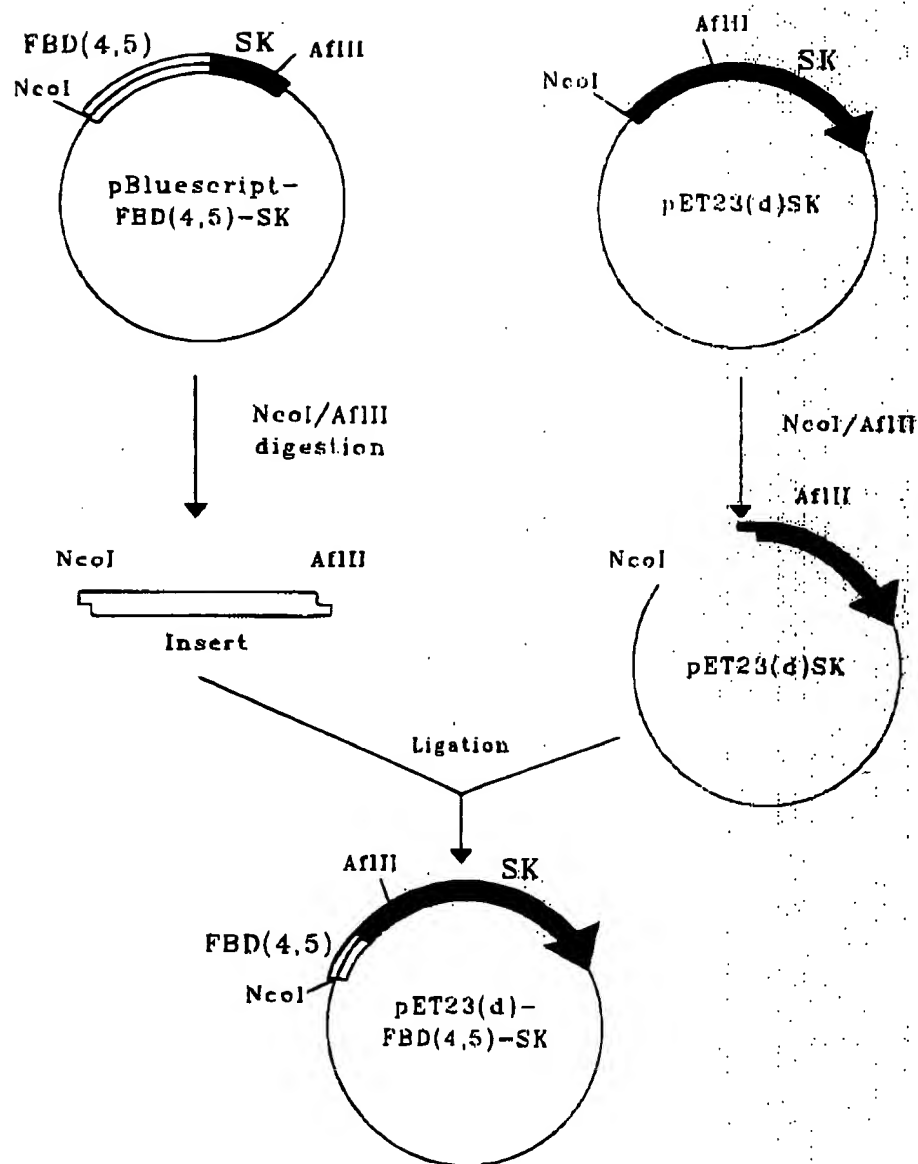
Fig. 21a

Fig. 21b

	10	20	30	40	50
1	TCGCTTCACG	TTCGCTCGCG	TATCGGTGAT	TCATTCTGCT	AACCAGTAAG
51	GCAACCCCGC	CAGCCTAGCC	GGGTCCTCAA	CGACAGGAGC	ACGATCATGC
101	GCACCCGTGG	CCAGGACCCA	ACGCTGCCCC	AGATCTCGAT	CCCGCGAAAT
151	TAATACGACT	CACTATAGGG	AGACCACAAC	GGTTTCCCTC	TAGAAATAAT
201	TTTGTTTAAC	TTTAAGAAGG	AGATATACCA	TGGTGCAAGC	ACAACAGATT
251	GTACCCATAG	CTGAGAAAGT	TTTTGATCAT	GCTGCTGGGA	CTTCCTATGT
301	GGTCGGAGAA	ACGTGGGAGA	AGGCAGCGGA	CGCATCACTT	GCACCTTCTAG
351	AAATAGATGC	AACGATCAGG	ACACAAGGAC	ATCCTATAGA	ATTGGAGACA
401	CCTGGAGCAA	GAAGGATAAT	CGAGGAAACC	TGCTCCAGTG	CATCTGCACA
451	GGCAACGGCC	GAGGAGAGTG	GAAGTGTGAG	AGGCACACCT	CTGTGCAGAC
501	CACATCGAGC	GGATCTGGCC	CCTTCACCGA	TGTTCTGATT	GCTGGACCTG
551	AGTGGCTGCT	AGACCGTCCA	TCTGTCAACA	ACAGCCAATT	GGTTGTTAGC
601	GTTGCTGGTA	CTGTTGAGGG	GACGAATCAA	GACATTAGTC	TTAAATTTTT
651	TGAAATCGAT	CTAACATCAC	GACCTGCTCA	TGGAGGAAAG	ACAGAGCAAG
701	GCTTAAGTCC	AAAATCAAAA	CCATTTGCTA	CTGATAGTGG	CGCGATGTCA
751	CATAAACTTG	AGAAAGCTGA	CTTACTAAAG	GCTATTCAAG	AACAATTGAT
801	CGCTAACGTC	CACAGTAACG	ACGACTACTT	TGAGGTCATT	GATTTTGCAA
851	GCGATGCAAC	CATTACTGAT	CGAAACGGCA	AGGTCTACTT	TGCTGACAAA
901	GATGGTTCGG	TAACCTTGCC	GACCCAACCT	GTCCAAGAAT	TTTTGCTAAG
951	CGGACATGTG	CGCGTTAGAC	CATATAAAGA	AAAACCAATA	CAAAACCAAG
1001	CGAAATCTGT	TGATGTGGAA	TATACTGTAC	AGTTTACTCC	CTTAAACCCCT
1051	GATGACGATT	TCAGACCAGG	TCTCAAAGAT	ACTAAGCTAT	TGAAAACACT
1101	AGCTATCGGT	GACACCATCA	CATCTCAAGA	ATTACTAGCT	CAAGCACAAA
1151	GCATTTTAAA	CAAAAACCAC	CCAGGCTATA	CGATTTATGA	ACGTGACTCC
1201	TCAATCGTCA	CTCATGACAA	TGACATTTTC	CGTACGATTT	TACCAATGGA
1251	TCAAGAGTTT	ACTTACCGTG	TTAAAAATCG	GGAACAAGCT	TATAGGATCA
1301	ATAAAAAATC	TGGTCTGAAT	GAAGAAATAA	ACAACACTGA	CCTGATCTCT
1351	GAGAAATATT	ACGTCCTTAA	AAAAGGGGAA	AAGCCGTATG	ATCCCTTTGA
1401	TCGCAGTCAC	TTGAAACTGT	TCACCATCAA	ATACGTTGAT	GTGATACCA
1451	ACGAATTGCT	AAAAAGTGAG	CAGCTCTTAA	CAGCTAGCGA	ACGTAACCTA
1501	GACTTCAGAG	ATTTATACGA	TCCTCGTGAT	AAGGCTAAAC	TACTCTACAA
1551	CAATCTCGAT	GCTTTTGGTA	TTATGGACTA	TACCTTAACT	GGAAAAGTAG
1601	AGGATAATCA	CGATGACACC	AACCGTATCA	TAACCGTTTA	TATGGGCAAG
1651	CGACCCGAAG	GAGAGAATGC	TAGCTATCAT	TTAGCCTATG	ATAAAGATCG
1701	TTATACCGAA	GAAGAACGAG	AAGTTTACAG	CTACCTGCGT	TATACAGGGA
1751	CACCTATACC	TGATAACCCCT	AACGACAAAT	AA	



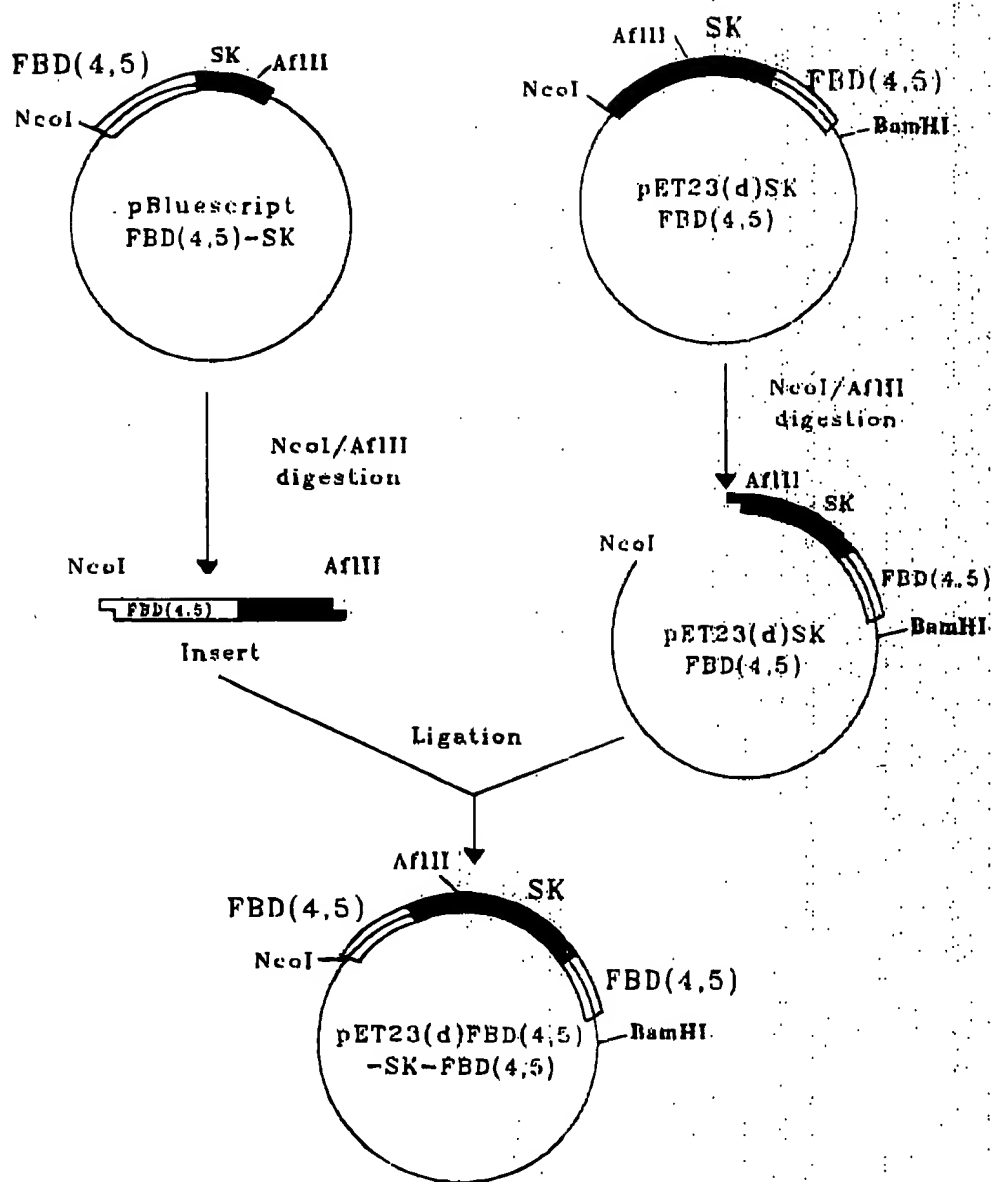
Fig. 22a

Fig. 22b

	10	20	30	40	50
1	CGAAGACCAT	TCATGTTGTT	GCTCAGGTGG	CAGACGTTTT	GCAGCAGCAG
51	TCGCTTCACG	TTCGCTCGCG	TATCGGTGAT	TCATTCTGCT	AACCAGTAAG
101	GCAACCCCGC	CAGCCTAGCC	GGGTCCTCAA	CGACAGGAGC	ACGATCATGC
151	GCACCCGTGG	CCAGGACCCA	ACGCTGCCCG	AGATCTCGAT	CCCGCGAAAT
201	TAATACGACT	CACTATAGGG	AGACCACAAC	GGTTTCCCTC	TAGAAATAAT
251	TTTGTTTAAC	TTTAAGAAGG	AGATATACCA	TGGTGCAAGC	ACAACAGATT
301	GTACCCATAG	CTGAGAAGTG	TTTTGATCAT	GCTGCTGGGA	CTTCCTATGT
351	GGTCGGAGAA	ACGTGGGAGA	AGGCAGCGGA	CGCATCACTT	GCACCTCTAG
401	AAATAGATGC	AACGATCAGG	ACACAAGGAC	ATCCTATAGA	ATTGGAGACA
451	CCTGGAGCAA	GAAGGATAAT	CGAGGAAACC	TGCTCCAGTG	CATCTGCACA
501	GGCAACGGCC	GAGGAGAGTG	GAAGTGTGAG	AGGCACACCT	CTGTGCAGAC
551	CACATCGAGC	GGATCTGGCC	CCTTCACCGA	TGTTTCGTATT	GCTGGACCTG
601	AGTGGCTGCT	AGACCGTCCA	TCTGTCAACA	ACAGCCAATT	GGTTGTTAGC
651	GTTGCTGGTA	CTGTTGAGGG	GACGAATCAA	GACATTAGTC	TTAAATTTTT
701	TGAAATCGAT	CTAACATCAC	GACCTGCTCA	TGGAGGAAAG	ACAGAGCAAG
751	GCTTAAGTCC	AAAATCAAAA	CCATTGCTA	CTGATAGTGG	CGCGATGTCA
801	CATAAACTTG	AGAAAGCTGA	CTTACTAAAG	GCTATTCAAG	AACAATTGAT
851	CGCTAACGTC	CACAGTAACG	ACGACTACTT	TGAGGTCATT	GATTITGCAA
901	GCGATGCAAC	CATTACTGAT	CGAAACGGCA	AGGTCTACTT	TGCTGACAAA
951	GATGGTTCGG	TAACCTTGCC	GACCCAACCT	GTCCAAGAAT	TTTTGCTAAG
1001	CGGACATGTG	CGCGTTAGAC	CATATAAAGA	AAAACCAATA	CAAAACCAAG
1051	CGAAATCTGT	TGATGTGGAA	TATACTGTAC	AGTTTACTCC	CTTAAACCTT
1101	GATGACGATT	TCAGACCAGG	TCTCAAAGAT	ACTAAGCTAT	TGAAAACACT
1151	AGCTATCGGT	GACACCATCA	CATCTCAAGA	ATTACTAGCT	CAAGCACAAA
1201	GCATTTTAAA	CAAAAACCAC	CCAGGCTATA	CGATTTATGA	ACGTGACTCC
1251	TCAATCGTCA	CTCATGACAA	TGACATTTTC	CGTACGATTT	TACCAATGGA
1301	TCAAGAGTTT	ACTTACCGTG	TTAAAAATCG	GGAACAAGCT	TATAGGATCA
1351	ATAAAAAATC	TGGTCTGAAT	GAAGAAATAA	ACAACACTGA	CCTGATCTCT
1401	GAGAAATATT	ACGTCCTTAA	AAAAGGGGAA	AAGCCGTATG	ATCCCTTTGA
1451	TCGCAGTCAC	TTGAAACTGT	TCACCATCAA	ATACGTTGAT	GTCGATACCA
1501	ACGAATTGCT	AAAAAGTGAG	CAGCTCTTAA	CAGCTAGCGA	ACGTAACCTA
1551	GACTTCAGAG	ATTTATACGA	TCCTCGTGAT	AAGGCTAAAC	TACTCTACAA
1601	CAATCTCGAT	GCTTTTGGTA	TTATGGACTA	TACCTTAACT	GGAAAAGTAG
1651	AGGATAATCA	CGATGACACC	AACCGTATCA	TAACCGTTTA	TATGGGCAAG
1701	CGACCCGAAG	GAGAGAATGC	TAGCTACCAT	TTAGCTGGTG	GTGGCCAGGC
1751	GCAACAGATT	GTACCCATAG	CTGAGAAGTG	TTTTGATCAT	GCTGCTGGGA
1801	CTTCCTATGT	GGTCGGAGAA	ACGTGGGAGA	AGCCCTACCA	AGGCTGGATG
1851	ATGGTAGATT	GTACTTGCCT	GGGAGAAGGC	AGCGGACGCA	TCACTTGACAC
1901	TTCTAGAAAT	AGATGCAACG	ATCAGGACAC	AAGGACATCC	TATAGAATTG
1951	GAGACACCTG	GAGCAAGAAG	GATAATCGAG	GAAACCTGCT	CCAGTGCAATC
2001	TGCACAGGCA	ACGGCCGAGG	AGAGTGGGAG	TGTGAGAGGC	ACACCTCTGT
2051	GCAGACCACA	TCGAGCGGAT	CTGGCCCCCTT	CACCGATGTT	CGTTAG

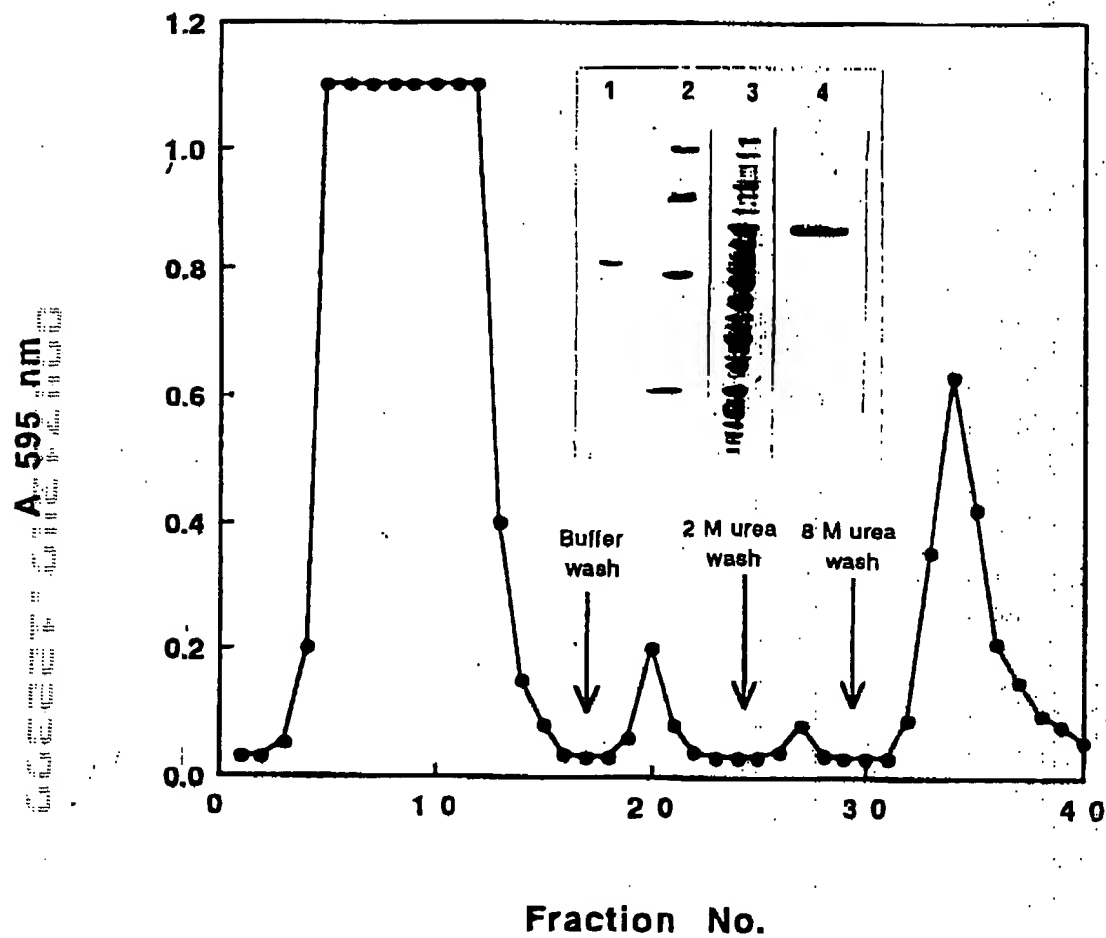
Fig. 23

Fig. 24